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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,633A

DATE: 02/12/2002

TIME: 10:08:41

Input Set : A:\sequence lsiti.txt

Output Set: N:\CRF3\02122002\I787633A.raw

ENTERED

3 <110> APPLICANT: Wilson, Robert JM  
4 Mullineaux, Conrad W  
5 Law, Anna E  
7 <120> TITLE OF INVENTION: Treatment of Infection  
9 <130> FILE REFERENCE: 117-347  
11 <140> CURRENT APPLICATION NUMBER: US/09/787,633A  
12 <141> CURRENT FILING DATE: 2001-07-10  
14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03180  
15 <151> PRIOR FILING DATE: 1999-09-22  
17 <150> PRIOR APPLICATION NUMBER: GB 9820658.4  
18 <151> PRIOR FILING DATE: 1998-09-22  
20 <160> NUMBER OF SEQ ID NOS: 7  
22 <170> SOFTWARE: PatentIn Ver. 2.1  
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25 <211> LENGTH: 1444  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Plasmodium falciparum  
29 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (26)..(1435)  
33 <220> FEATURE:  
34 <221> NAME/KEY: misc\_feature  
35 <222> LOCATION: (1276)  
36 <223> OTHER INFORMATION: h represents A, T or C  
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40 Met Ile Lys Leu Lys Asn Phe Leu Asn  
41 1 5  
43 att tat aat tta aat tat aaa tat caa tat aaa aat aaa ata aat tta 100  
44 Ile Tyr Asn Leu Asn Tyr Lys Tyr Gln Tyr Lys Asn Lys Ile Asn Leu  
45 10 15 20 25  
47 tat tta ata aga caa gga tta aat ata aat tta ata aaa aat tta tct 148  
48 Tyr Leu Ile Arg Gln Gly Leu Asn Ile Asn Leu Ile Lys Asn Leu Ser  
49 30 35 40  
51 agt aat att ttt tta tat atg ttt att tat aat ttt aaa aaa tat tct 196  
52 Ser Asn Ile Phe Leu Tyr Met Phe Ile Tyr Asn Phe Lys Lys Tyr Ser  
53 45 50 55  
55 tta aaa tta tta aat ata ttt aaa tta cct gat tgg aat ttt ttt gat 244  
56 Leu Lys Leu Leu Asn Ile Phe Lys Leu Pro Asp Trp Asn Phe Phe Asp  
57 60 65 70  
59 tgt cca aat ata aat tat gat aat att att tat tat tct tct att tta 292  
60 Cys Pro Asn Ile Asn Tyr Asp Asn Ile Ile Tyr Tyr Ser Ser Ile Leu  
61 75 80 85

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63 aaa gat aat aat tta ata tat tat tta aaa aat aat tta aat att gaa 340
64 Lys Asp Asn Asn Leu Ile Tyr Tyr Leu Lys Asn Asn Leu Asn Ile Glu
65 90 95 100 105
67 ttt tta gat agt ata tta ata aaa aat aat tct ata gat att ata ttt 388
68 Phe Leu Asp Ser Ile Leu Ile Lys Asn Asn Ser Ile Asp Ile Ile Phe
69 110 115 120
71 gat agt atg tct att tta cat act aca caa tat ttt tta aaa aaa tth 436
W--> 72 Asp Ser Met Ser Ile Leu His Thr Thr Gln Tyr Phe Leu Lys Lys Xaa
73 125 130 135
75 gga ata att ttt tta cct tta ttt gat att ata ttt aaa tat cct tta 484
76 Gly Ile Ile Phe Leu Pro Leu Phe Asp Ile Ile Phe Lys Tyr Pro Leu
77 140 145 150
79 tta ata aaa aaa tat tta ggt act att att tct tat aaa gat aat ttt 532
80 Leu Ile Lys Lys Tyr Leu Gly Thr Ile Ile Ser Tyr Lys Asp Asn Phe
81 155 160 165
83 ttt gct aat att aat tca ata ata ttt agt gaa gga tct ttt tgt tat 580
84 Phe Ala Asn Ile Asn Ser Ile Ile Phe Ser Glu Gly Ser Phe Cys Tyr
85 170 175 180 185
87 ata cct aaa tat gta aag tgt aat ttt aat tta tca aca tat ttt aaa 628
88 Ile Pro Lys Tyr Val Lys Cys Asn Phe Asn Leu Ser Thr Tyr Phe Lys
89 190 195 200
91 act aat tct tct gat ttt gca caa ttt gaa cgt act tta ata ata gtt 676
92 Thr Asn Ser Ser Asp Phe Ala Gln Phe Glu Arg Thr Leu Ile Ile Val
93 205 210 215
95 ggt aaa tat tct tat gta tca tat tta gaa gga tgt aca gct tca tta 724
96 Gly Lys Tyr Ser Tyr Val Ser Tyr Leu Glu Gly Cys Thr Ala Ser Leu
97 220 225 230
99 tat aaa gaa tca caa tta cat gta gct ata gta gaa ata ata gta aaa 772
100 Tyr Lys Glu Ser Gln Leu His Val Ala Ile Val Glu Ile Ile Val Lys
101 235 240 245
103 gat tat ggt tat ata aaa tat tat aca tta caa aat tgg tat aga gga 820
104 Asp Tyr Gly Tyr Ile Lys Tyr Tyr Thr Leu Gln Asn Trp Tyr Arg Gly
105 250 255 260 265
107 gat tat tta ggt aat ggt ggt tta tat aat ttt aca act aaa cgt ggt 868
108 Asp Tyr Leu Gly Asn Gly Gly Leu Tyr Asn Phe Thr Thr Lys Arg Gly
109 270 275 280
111 ata tgt tta aat tat tca aaa tta gat tgg ata caa gtt gaa gta ggt 916
112 Ile Cys Leu Asn Tyr Ser Lys Leu Asp Trp Ile Gln Val Glu Val Gly
113 285 290 295
115 tcg att ata aca tgg aaa tac cct tct act att tta aaa ggt aaa ttt 964
116 Ser Ile Ile Thr Trp Lys Tyr Pro Ser Thr Ile Leu Lys Gly Lys Phe
117 300 305 310
119 tct att agt aat ttt tat tca ata tct ttt ata tca aat atg caa ata 1012
120 Ser Ile Ser Asn Phe Tyr Ser Ile Ser Phe Ile Ser Asn Met Gln Ile
121 315 320 325
123 gct gat act ggt agt aaa atg tat cat ata gga tct tat act aaa agt 1060
124 Ala Asp Thr Gly Ser Lys Met Tyr His Ile Gly Ser Tyr Thr Lys Ser
125 330 335 340 345
127 tat ata att tct aaa agt ata tct tta aat aac tca tta aat ata ttt 1108

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128 Tyr Ile Ile Ser Lys Ser Ile Ser Leu Asn Asn Ser Leu Asn Ile Phe
129                               350                               355                               360
131 aga ggt tta gta tat att aaa cct ttt tca tat aaa tct tat aat tat 1156
132 Arg Gly Leu Val Tyr Ile Lys Pro Phe Ser Tyr Lys Ser Tyr Asn Tyr
133                               365                               370                               375
135 act gaa tgt agt tct tta ata ttt ggt aat aat tct tta aca gta act 1204
136 Thr Glu Cys Ser Ser Leu Ile Phe Gly Asn Asn Ser Leu Thr Val Thr
137                               380                               385                               390
139 att cct tat ata aaa aat tat aat aat act agt tat gta aaa caa gaa 1252
140 Ile Pro Tyr Ile Lys Asn Tyr Asn Asn Thr Ser Tyr Val Lys Gln Glu
141                               395                               400                               405
143 gct ttt gtt tct aaa att gaa ath ata tat tta ttt tta tta atg caa 1300
144 Ala Phe Val Ser Lys Ile Glu Ile Ile Tyr Leu Phe Leu Leu Met Gln
145 410                               415                               420                               425
147 cgt ggt tta agt att tca gag tct att tca tta tta att ata ggt ttt 1348
148 Arg Gly Leu Ser Ile Ser Glu Ser Ile Ser Leu Leu Ile Ile Gly Phe
149                               430                               435                               440
151 tgt tct gat att tat aat aaa tta ccg ttt gaa ttt aat tta gag ata 1396
152 Cys Ser Asp Ile Tyr Asn Lys Leu Pro Phe Glu Phe Asn Leu Glu Ile
153                               445                               450                               455
155 cct ata tta ttt tca tta aaa att aaa gat ata ttt aat taattaaat 1444
156 Pro Ile Leu Phe Ser Leu Lys Ile Lys Asp Ile Phe Asn
157                               460                               465                               470
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 1443
163 <212> TYPE: DNA
164 <213> ORGANISM: Synechocystis PCC6803
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(1443)
170 <400> SEQUENCE: 2
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173 1                               5                               10                               15
175 ggc ttt gtc acc aac att gaa gcg gat gct atc ccc cgt ggt ctg agt 96
176 Gly Phe Val Thr Asn Ile Glu Ala Asp Ala Ile Pro Arg Gly Leu Ser
177                               20                               25                               30
179 gaa gac gtg gtg cga ctc att tct gct aag aaa aat gaa ccc gaa ttc 144
180 Glu Asp Val Val Arg Leu Ile Ser Ala Lys Lys Asn Glu Pro Glu Phe
181                               35                               40                               45
183 atg ttg gat ttt cgc ctc cgg gcc tac cgg cat tgg ctg acc atg gcg 192
184 Met Leu Asp Phe Arg Leu Arg Ala Tyr Arg His Trp Leu Thr Met Ala
185                               50                               55                               60
187 gaa ccc act tgg ccg gcg gtg cat tat ccc ccc att gat tac caa gat 240
188 Glu Pro Thr Trp Pro Ala Val His Tyr Pro Pro Ile Asp Tyr Gln Asp
189 65                               70                               75                               80
191 att att tac tac tcc gcc cct aag caa agt aag aaa aaa cta gaa agc 288
192 Ile Ile Tyr Tyr Ser Ala Pro Lys Gln Ser Lys Lys Lys Leu Glu Ser
193                               85                               90                               95

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195	tta	gat	gaa	gtg	gac	cca	gct	ttg	ttg	gaa	acc	ttt	gaa	aaa	tta	ggg	336
196	Leu	Asp	Glu	Val	Asp	Pro	Ala	Leu	Leu	Glu	Thr	Phe	Glu	Lys	Leu	Gly	
197				100					105					110			
199	att	ccc	cta	tcg	gag	caa	aaa	cgt	tta	agt	aat	gtg	gcg	gta	gat	gcc	384
200	Ile	Pro	Leu	Ser	Glu	Gln	Lys	Arg	Leu	Ser	Asn	Val	Ala	Val	Asp	Ala	
201			115					120						125			
203	att	ttt	gac	agt	gtt	tcc	att	ggc	aca	act	ttt	aag	gaa	aag	cta	gcg	432
204	Ile	Phe	Asp	Ser	Val	Ser	Ile	Gly	Thr	Thr	Phe	Lys	Glu	Lys	Leu	Ala	
205			130					135						140			
207	gaa	gac	ggg	gta	att	ttc	tgt	tct	att	tct	gaa	gca	ttg	cag	gaa	cat	480
208	Glu	Asp	Gly	Val	Ile	Phe	Cys	Ser	Ile	Ser	Glu	Ala	Leu	Gln	Glu	His	
209	145					150					155					160	
211	ccc	gac	ctg	gtg	caa	aaa	tat	ttg	ggc	agt	gtg	gtg	ccc	acc	gcc	gac	528
212	Pro	Asp	Leu	Val	Gln	Lys	Tyr	Leu	Gly	Ser	Val	Val	Pro	Thr	Ala	Asp	
213					165					170					175		
215	aac	ttc	ttt	gcc	gcc	tta	aac	tct	gct	gta	ttt	agt	gac	ggt	tcc	ttt	576
216	Asn	Phe	Phe	Ala	Ala	Leu	Asn	Ser	Ala	Val	Phe	Ser	Asp	Gly	Ser	Phe	
217			180						185					190			
219	gtt	ttt	att	ccc	aaa	ggg	gtg	aag	tgt	ccc	atg	gaa	ttg	tcc	acc	tat	624
220	Val	Phe	Ile	Pro	Lys	Gly	Val	Lys	Cys	Pro	Met	Glu	Leu	Ser	Thr	Tyr	
221			195					200						205			
223	ttc	cgc	att	aat	aat	ggg	gat	acg	ggg	cag	ttt	gag	cgg	aca	tta	att	672
224	Phe	Arg	Ile	Asn	Asn	Gly	Asp	Thr	Gly	Gln	Phe	Glu	Arg	Thr	Leu	Ile	
225			210				215							220			
227	att	gcc	gaa	gaa	ggg	gct	tcc	gtt	agc	tat	ttg	gaa	ggt	tgt	act	gcg	720
228	Ile	Ala	Glu	Glu	Gly	Ala	Ser	Val	Ser	Tyr	Leu	Glu	Gly	Cys	Thr	Ala	
229	225					230					235					240	
231	ccc	atg	tat	gac	acc	aat	caa	ctt	cat	gcg	gcg	gtg	gtg	gaa	ttg	gta	768
232	Pro	Met	Tyr	Asp	Thr	Asn	Gln	Leu	His	Ala	Ala	Val	Val	Glu	Leu	Val	
233					245					250					255		
235	gct	cta	gat	aat	gct	gac	att	aaa	tat	tcc	acc	gta	caa	aac	tgg	tac	816
236	Ala	Leu	Asp	Asn	Ala	Asp	Ile	Lys	Tyr	Ser	Thr	Val	Gln	Asn	Trp	Tyr	
237				260					265					270			
239	gct	ggg	gac	gaa	aat	ggc	aag	ggc	gga	att	tac	aac	ttt	gtg	act	aaa	864
240	Ala	Gly	Asp	Glu	Asn	Gly	Lys	Gly	Gly	Ile	Tyr	Asn	Phe	Val	Thr	Lys	
241			275					280						285			
243	cgg	ggt	cta	tgt	aaa	gga	gtt	aat	tcc	aaa	att	tcc	tgg	acc	caa	gta	912
244	Arg	Gly	Leu	Cys	Lys	Gly	Val	Asn	Ser	Lys	Ile	Ser	Trp	Thr	Gln	Val	
245			290				295					300					
247	gaa	acc	ggt	tcc	gcc	att	acc	tgg	aaa	tac	ccc	agt	tgt	gtg	cta	gtt	960
248	Glu	Thr	Gly	Ser	Ala	Ile	Thr	Trp	Lys	Tyr	Pro	Ser	Cys	Val	Leu	Val	
249	305					310					315					320	
251	ggg	gat	aat	tcc	gtc	ggg	gaa	ttc	tac	tct	att	gct	tta	act	aac	aac	1008
252	Gly	Asp	Asn	Ser	Val	Gly	Glu	Phe	Tyr	Ser	Ile	Ala	Leu	Thr	Asn	Asn	
253					325					330					335		
255	aaa	cag	caa	gct	gat	acg	gga	act	aaa	atg	att	cac	atc	ggt	aaa	aat	1056
256	Lys	Gln	Gln	Ala	Asp	Thr	Gly	Thr	Lys	Met	Ile	His	Ile	Gly	Lys	Asn	
257				340						345				350			
259	acc	cgt	agt	atc	att	att	tcc	aaa	ggc	att	tcc	gct	ggt	aat	tcc	gcc	1104

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260 Thr Arg Ser Ile Ile Ile Ser Lys Gly Ile Ser Ala Gly Asn Ser Ala
261          355          360          365
263 aac agt tac cgg ggt ttg gtg aaa atg gga cct aaa gcc cag ggc gct 1152
264 Asn Ser Tyr Arg Gly Leu Val Lys Met Gly Pro Lys Ala Gln Gly Ala
265          370          375          380
267 cgc aat tat tcc cag tgt gat tcc atg ctc att ggc gat cgg gca gcg 1200
268 Arg Asn Tyr Ser Gln Cys Asp Ser Met Leu Ile Gly Asp Arg Ala Ala
269 385          390          395          400
271 gct aat act ttt ccc tat att caa gtg gac aat aat acc gcc aaa gta 1248
272 Ala Asn Thr Phe Pro Tyr Ile Gln Val Asp Asn Asn Thr Ala Lys Val
273          405          410          415
275 gaa cat gaa gct tcc act tcc aaa att ggc gag gat caa ctc ttt tac 1296
276 Glu His Glu Ala Ser Thr Ser Lys Ile Gly Glu Asp Gln Leu Phe Tyr
277          420          425          430
279 ttt gcc caa cgg gga att tct gag gaa gat gcg gtg tcc atg cta gtc 1344
280 Phe Ala Gln Arg Gly Ile Ser Glu Glu Asp Ala Val Ser Met Leu Val
281          435          440          445
283 agc ggt ttc tgt aag gat gtg cta aac gaa tta ccc atg gaa ttt gcg 1392
284 Ser Gly Phe Cys Lys Asp Val Leu Asn Glu Leu Pro Met Glu Phe Ala
285          450          455          460
287 gcg gag gct gat aaa tta ctg agt ctc aaa cta gaa ggt act gtg ggt 1440
288 Ala Glu Ala Asp Lys Leu Leu Ser Leu Lys Leu Glu Gly Thr Val Gly
289 465          470          475          480
291 taa 1443
295 <210> SEQ ID NO: 3
296 <211> LENGTH: 1527
297 <212> TYPE: DNA
298 <213> ORGANISM: Escherichia coli
300 <220> FEATURE:
301 <221> NAME/KEY: CDS
302 <222> LOCATION: (1)..(1527)
304 <400> SEQUENCE: 3
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306 Met Trp Leu Trp Arg Lys Leu Trp Gly Ile Gly Gly Thr Met Ser Arg
307 1          5          10          15
309 aat act gaa gca act gac gat gtc aaa acc tgg acc ggc ggc ccg ctg 96
310 Asn Thr Glu Ala Thr Asp Asp Val Lys Thr Trp Thr Gly Gly Pro Leu
311          20          25          30
313 aat tat aaa gaa gga ttc ttc acc cag tta gcc acc gat gag ctg gca 144
314 Asn Tyr Lys Glu Gly Phe Phe Thr Gln Leu Ala Thr Asp Glu Leu Ala
315          35          40          45
317 aag ggg ata aac gaa gag gtg gtg cgc gca att tcg gcg aag cgt aat 192
318 Lys Gly Ile Asn Glu Glu Val Val Arg Ala Ile Ser Ala Lys Arg Asn
319          50          55          60
321 gag ccg gag tgg atg ctg gag ttt cgt cta aac gcc tat cgc gca tgg 240
322 Glu Pro Glu Trp Met Leu Glu Phe Arg Leu Asn Ala Tyr Arg Ala Trp
323 65          70          75          80
325 ctg gag atg gaa gaa ccg cac tgg ttg aaa gcg cac tac gac aag ctg 288
326 Leu Glu Met Glu Glu Pro His Trp Leu Lys Ala His Tyr Asp Lys Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/787,633A

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Input Set : A:\sequence lsiti.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1